

**My Model of Character Evolution and Site Variance determined by MEGA was HKY + G.**

**The following are the input parameters that I had for BEAUti:**

Partitions Taxa Tips Traits Sites Clocks Trees States Priors Operators **MCMC**

Length of chain: 10000000

Echo state to screen every: 1000

Log parameters every: 1000

File name stem: APOE Alignment - MUSCLE.nxs

☒ Add .bt suffix

Log file name: APOE Alignment - MUSCLE.nxs.log.txt

Trees file name: APOE Alignment - MUSCLE.nxs.trees

☐ Create tree log file with branch length in substitutions:

Substitutions trees file name:

☒ Create operator analysis file:

Operator analysis file name: APOE Alignment - MUSCLE.nxs.ops.txt

☐ Sample from prior only - create empty alignment

Partitions Taxa Tips Traits Sites Clocks Trees States **Priors** Operators MCMC

☐ Use classic priors/operators

Parameter	Prior	Bound	Description
CP1.kappa	* LogNormal [1, 1.25], initial=2	[0, ∞]	HKY transition-transversion parameter for codon position 1
CP2.kappa	* LogNormal [1, 1.25], initial=2	[0, ∞]	HKY transition-transversion parameter for codon position 2
CP3.kappa	* LogNormal [1, 1.25], initial=2	[0, ∞]	HKY transition-transversion parameter for codon position 3
CP1.frequencies	* Dirichlet [1,1]	[0, ∞]	base frequencies for codon position 1
CP2.frequencies	* Dirichlet [1,1]	[0, ∞]	base frequencies for codon position 2
CP3.frequencies	* Dirichlet [1,1]	[0, ∞]	base frequencies for codon position 3
CP1.alpha	* Exponential [0.5], initial=0.5	[0, ∞]	gamma shape parameter for codon position 1
CP2.alpha	* Exponential [0.5], initial=0.5	[0, ∞]	gamma shape parameter for codon position 2
CP3.alpha	* Exponential [0.5], initial=0.5	[0, ∞]	gamma shape parameter for codon position 3
allNus	* Dirichlet [1,1]	[0, ∞]	relative rates amongst partitions parameter
clock.rate	* Fixed value, value=1	[0, ∞]	substitution rate
treeModel.rootHeight	* Using Tree Prior in [0, ∞]	[0, ∞]	root height of the tree
constant.popSize	* 1/x, initial=1	[0, ∞]	coalescent population size parameter

Substitution Model

default

Nucleotide Substitution Model - default

Substitution Model: HKY

Base frequencies: Estimated

Site Heterogeneity Model: Gamma

Number of Gamma Categories: 4

Partition into codon positions: 3 partitions: positions 1, 2, 3

Link/Unlink parameters:

- ☒ Unlink substitution rate parameters across codon positions
- ☒ Unlink rate heterogeneity model across codon positions
- ☒ Unlink base frequencies across codon positions

Use Yang96 model

Use SRD06 model

☒ Link tree prior for all trees

Trees

default

Tree prior shared by all tree models

Tree Prior: Coalescent: Constant Size

Citation: Kingman JFC (1982) Stoch Proc Appl 13, 235-248 [Constant Coalescent].

Tree Model - default

☐ Random starting tree

☒ UPGMA starting tree

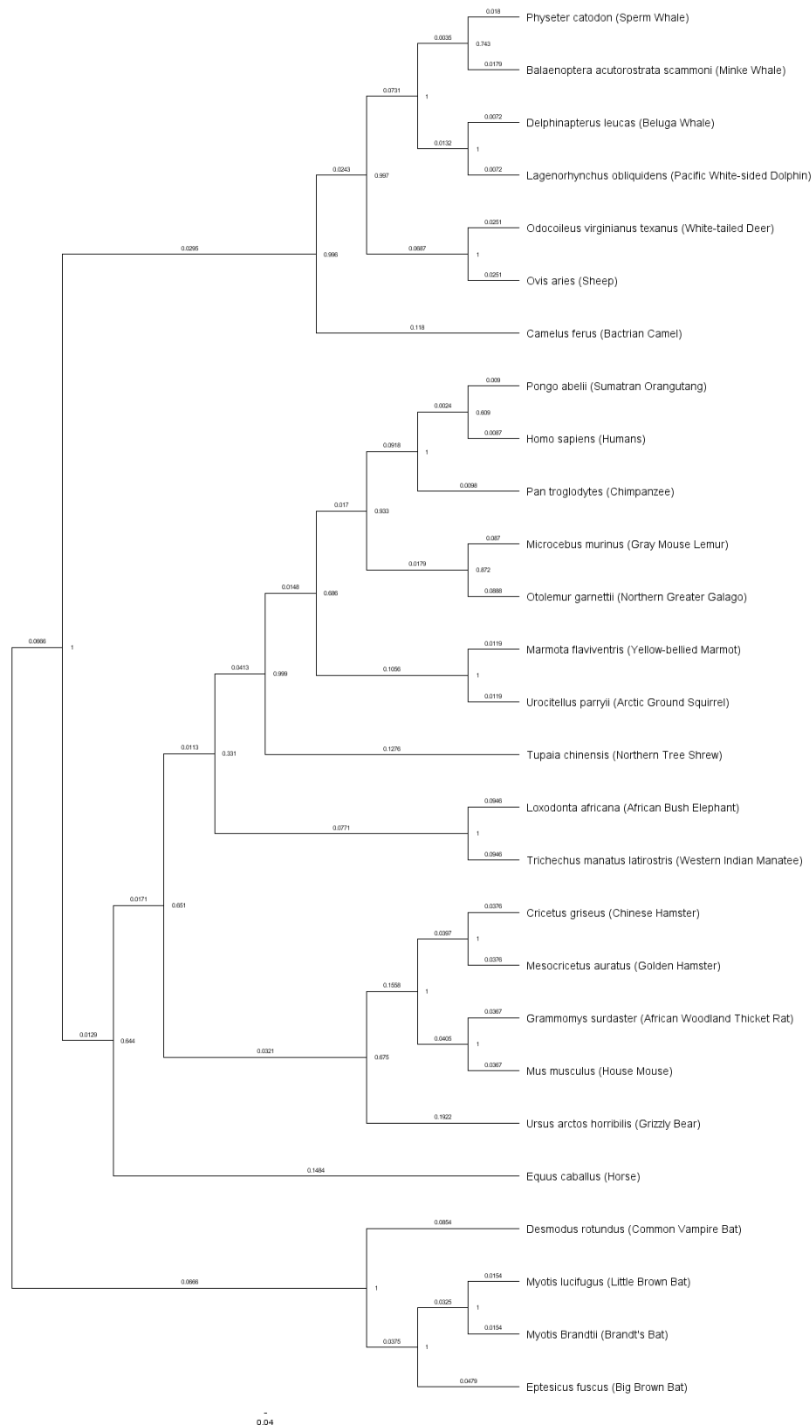
☐ User-specified starting tree

Select user-specified tree: no tree loaded

Export format for tree: Newick

Import user-specified starting trees from **NEXUS** format data files using the 'Import Data' menu option. Trees must be rooted and strictly bifurcating (binary).

## My final Bayesian Tree edited using FigTree:



Included in my Bayesian Tree are raw branch lengths that are scaled to their length (located above each branch) and posterior node probability (located to the right of each node). My Bayesian Tree compared to my ML and MP trees is actually pretty similar. The only difference that I could find was that the placement of *Ursus arctos horribilis* in my Bayesian tree was placed in a clade with *Cricetus griseus*, etc. as opposed to being a polytomy in both my MP and ML trees. This also leads to a

difference in the grouping of the *Cricetulus griseus* clade being further removed from the *Marmota flaviventris* clade. Much like my MP and ML trees, it differs pretty significantly from my NJ tree in the amount of polytomies present in the NJ tree compared to the Bayesian tree. Considering that my Bayesian tree is most similar to MP and ML, I think that is safe to consider either my MP or my Bayesian tree as my “best” tree to base my observations on. I rooted my Bayesian tree using my four bat species located at the bottom.